

### **Rejection under 35 U.S.C. 101**

The Examiner rejects claims 1-7 under 35 U.S.C. 101 on the ground that the claimed truncated glucanases can exist in nature. Applicants have amended claims by canceling claims 1-7 and adding new claims 20-24. New claims 20-24 include language "An isolated truncated glucanase" following the Examiner's suggestion, which explicitly excludes any naturally occurring glucanases. Accordingly, the rejection under 35 U.S.C. 101 has been overcome and should be withdrawn.

### **Rejection under 35 U.S.C. 112, second paragraph**

The Examiner rejects claims 1-7 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicants regard as the invention. Specifically, the Examiner stated that it is unclear which amino acids are encompassed as being substantially identical to a portion of the wild-type glucanase.

Claims 1-7 have been removed from consideration. The new independent claim 20 is directed to a truncated glucanase having amino acid residues between 246 to 321, in which at least 246 amino acids of the sequence starting at amino acid residue 5 and extending therefrom is substantially identical to a portion of the amino acid of the wild-type glucanase starting from amino acid residue 1.

Supports for the new claim 20 can be found in SEQ ID No: 1, SEQ ID No: 2 and SEQ ID No: 3 in the Sequencing Listing.

The term "substantially identical" is explained in the specification from page 10, line 18 to page 11, line 2.

Accordingly, new claims 20-24 are now definite and clear. The rejection under 35 U.S.C. 112, second paragraph, has been overcome and should be withdrawn.

**Rejection under 35 U.S.C. 102(e)**

The Examiner rejects claims 1-3 and 6-7 under 35 U.S.C. 102(e) as being anticipated by Li et al. (U.S. Pat. No. 6,103,511). More specifically, the Examiner considers the SEQ ID No: 12 in Li et al. is encompassed by claim 1.

Applicants note that claims 4, and claim 5, which depends on claim 4, are not rejected by the Examiner on this ground.

Applicants have removed claims 1-7 from consideration and added new claims 20-24, in which claim 20 is the only dependent claim. The newly added claims 20-24 essentially incorporate the elements of the cancelled claim 4, thereby no longer being anticipated by Li et al.

Li et al. discloses an amino acid sequence, i.e. SEQ ID No: 12, that is a truncated form of glucanase sequence from *Fibrobacter succinogene*. This truncated glucanase sequence includes a 27 amino acid signal peptide and the N-terminal plus the first 221 amino acid residues of the wild-type glucanase. The wild type glucanase normally has total 349 amino acid residues, as shown by Li et al. In addition, the truncation of Li et al. does not include any PXSSSS sequence.

Most importantly, Li et al. did not report any activity of this truncated glucanase. In fact, applicants have found that this truncated form of the glucanase has no activity at all (Applicants will provide evidence by a declaration if the Examiner requests).

In contrast, the present invention, as claimed in new claim 20, is directed to a novel truncation of the wild-type glucanase, where the activity of the glucanase is enhanced when the truncated glucanase also contains at least 25 amino acids more than the truncated form of the glucanase described by Li et al. at the C-terminal. The present truncation results in a sequence having at least 246 amino acids including a PXSSSS sequence substantially identical to a corresponding portion of the wild type glucanase.

Thus, the truncated glucanase of the present invention structurally and functionally differs from the truncated form of the glucanase taught by Li et al. The attached is a comparison between the claimed sequence and the Li et al.'s sequences, where "PCR-TF-Glu" represents the claimed sequence, "SEQ ID No 12" represents the truncated form of the glucanase from *Fibrobacter succinogene* disclosed by Li et al. and "Lic A sequen" represents the fungal glucanase disclosed by Li et al.

More importantly, the present truncation results in a glucanase having enhanced enzymatic activity whereas Li et al.'s truncated glucanase is inactive.

Thus, Li et al. fails to teach each and every element of the present invention as encompassed by new claims 20-24. The present invention cannot be anticipated by Li. et al.. Accordingly, the rejection under 35 U.S.C. 102(e) has been overcome and should be withdrawn.

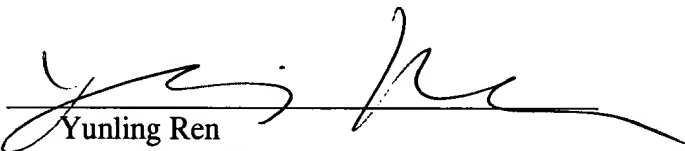
Allowance of claims 20-24 is respectfully requested.

Any additional fees or charges required at this time in connection with the application may be charged to our Patent and Trademark Office Deposit Account No. 03-2412.

Respectfully submitted,

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By

A handwritten signature in black ink, appearing to read 'Yunling Ren', is written over a horizontal line.

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AMENDMENTS TO THE SPECIFICATION AND CLAIMS SHOWING CHANGES

IN THE CLAIMS:

20. (new) An isolated truncated glucanase having enhanced glucanase activity and an amino acid sequence of a total number of amino acid residues between 246 to 321, wherein a portion of said sequence containing at least 246 amino acid residues starting at amino acid residue 5 and extending therefrom is substantially identical to a corresponding portion of the amino acid sequence of a wild-type glucanase from *Fibrobacter succinogene*, said corresponding portion of the amino acid sequence of said wild-type glucanase starting at amino acid residue 1 of said amino acid sequence of said wild-type glucanase and extending therefrom.

21. (new) The isolated truncated glucanase of claim 20, absent a repeated PXSSSS segment, wherein X represents an uncharged amino acid residue.

22. (new) The isolated truncated glucanase of claim 20, wherein said amino acid sequence of said wild-type glucanase is identical to SEQ ID No: 3.

23. (new) The isolated truncated glucanase of claim 20 having an amino acid sequence substantially identical to SEQ ID No: 1.

24. (new) The isolated truncated glucanase of claim 20 having an amino acid sequence substantially identical to SEQ ID No: 2.

PCR-TF-Glu ~~~~~~  
 SEQ ID NO 12 ~~~~~~  
 Lic A sequen MKSIISIAAL SVLGLISKTM AAPAPAPVPG TAWNGSHDVM DFNYESNRF 50

PCR-TF-Glu ~~~~~~ ~MVSAKDFSG AELYTLEEVQ 19  
 SEQ ID NO 12 ~~~~~~MN IKKTAVKSAL AVAAAAAALT TNVSAKDFSG AELYTLEEVQ 42  
 Lic A sequen EMSNWPNGEM FNCRWTPNND KFENGKLKLT IDRDGSGYTC GEYRTKNYYG 100

PCR-TF-Glu YGKFARMKM AAASGTVSSM FLYQNGSEIA DGRPWEVDI EVLGKNPGSF 69  
 SEQ ID NO 12 YGKFARMKM AAASGTVSSM FLYQNGSEIA DGRPWEVDI EVLGKNPGSF 92  
 Lic A sequen YGMFQVNMKP IKNPGVVSSF FTYTGPS... DGTKWDEIDI EFLGYDTTKV 147

PCR-TF-Glu QSNIIITGKAG AQKTSEKHHA VSPAADQAFH TYGLEWTPNY VRWTVDGQEV 119  
 SEQ ID NO 12 QSNIIITGKAG AQKTSEKHHA VSPAADQAFH TYGLEWTPNY VRWTVDGQEV 142  
 Lic A sequen QFNYYTNGQG HH...EHIHY LGFDASQGFH TYGFFWARS ITWYVDGTAV 194

PCR-TF-Glu RKTEGGQVSN LTGTQG.LRF NLWSSESA.A WVGQFDESKL PLFQFINWVK 167  
 SEQ ID NO 12 RKTEGGQVSN LTGTQG.LRF NLWSSESA.A WVGQFDESKL PLFQFINWVK 190  
 Lic A sequen YTA....YDN IPDTPGKIMM NAWNGIGVDD WLRPFN.GRT NISAYYDWVS 239

PCR-TF-Glu VYKYTPGQGE GGSDFTLDWT DNFDTFDGSR WGKGDWTFDG NRVDLTDKNI 217  
 SEQ ID NO 12 VYKYTPGQGE GGSDFTLDWT DNFDTFDGSR WGKGDWTF~~ ~~~~~~ 228  
 Lic A sequen .YD.APRN~ ~~~~~~ ~~~~~~ ~~~~~~ 245

PCR-TF-Glu YSRDGM LILA LTRKGQESFN GQVPRDDEPA PNSSSVDKLA AALEHHHHHH 267  
 SEQ ID NO 12 ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~  
 Lic A sequen ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~ ~~~~~~

**Figure 3. Protein sequence alignment of the truncated *Fibrobacter succinogenes* 1,3-1,4- $\beta$ -D glucanases and the fungal glucanase (Lic A) disclosed in Li et al. patent.**

Identical amino acid residues are denoted as shaded. The sequence identity between PCR-TF-glucanase and Lic A glucanase of Li et al are approximately 30%.